

An Adaptive Graph Neural Network Framework for Accurate Brain Tumor Detection and Segmentation from MRI Images

T. R. Thirumavalavan¹, S.Karunanithi²

Abstract: Brain tumor diagnosis from magnetic resonance imaging (MRI) remains a challenging task due to the presence of noise, complex tumor structures, and high-dimensional image features. Accurate detection and classification are essential for effective clinical decision-making and treatment planning. To address these challenges, this study proposes a novel RGCS-NCGNN-AAM framework for automated brain tumor analysis. The proposed approach integrates advanced preprocessing, dimensionality reduction, segmentation, classification, and optimization techniques into a unified pipeline. Initially, MRI images are enhanced using a LABF-based preprocessing method to suppress noise while preserving important structural information. Subsequently, Spatially Driven Principal Component Analysis (SD-PCA) is employed to reduce feature dimensionality and retain discriminative tumor-related characteristics. For precise tumor localization, a LA-ST segmentation technique is introduced to accurately delineate tumor boundaries and improve region extraction. The segmented features are then processed through a Robust Graph Convolution Structure-based Neural Context Graph Neural Network (RGCS-NCGNN), which effectively captures both topological and semantic relationships among data samples. Furthermore, an Adaptive Altruistic Mutualism (AAM) optimization strategy is incorporated to dynamically adjust model parameters and enhance learning performance. The proposed framework was evaluated using benchmark brain tumor MRI datasets and demonstrated superior performance in terms of classification accuracy, segmentation quality, and model robustness. Experimental results indicate that the integration of graph-based learning and adaptive optimization significantly improves diagnostic reliability compared with conventional machine learning and deep learning approaches. In addition, the framework preserves critical spatial information, enabling more accurate tumor characterization and boundary identification. The proposed method also exhibits strong scalability and generalization capabilities across diverse MRI samples. These findings suggest that the RGCS-NCGNN-AAM framework can serve as an effective computer-aided diagnostic tool for supporting radiologists and healthcare professionals in brain tumor assessment. Future research will focus on incorporating quantum graph neural networks and self-supervised learning techniques to further enhance computational efficiency and diagnostic performance in real-world clinical environments.

Introduction

Residual Group Channel and Space Non-Convolutional Graph Neural Network (RGCS-NCGNN) is a unified architecture that combines Residual Group Channel and Space Attention Network (RGCSA) [18] and Non-Convolutional Graph Neural Network (NCGNN) [21]. RGCS-NCGNN is employed to classify MRI images into Tumor and Non-Tumor. This technique integrates residual connections with spatial and channel attention modules to improve feature learning.

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While removing unnecessary features, it successfully identifies tumor-relevant areas [7]. RGCSA enhances classification accuracy by focusing attention on most informative spatial and channel features while suppressing irrelevant noise. The generator (RGCSA) is encouraged by adversarial loss to provide outputs that are identical to actual tumor detections by a discriminator. During training, it directs network to acquire accurate and realistic tumor class represented as,

$$L_{adv} = F_{y,z}[\log \log E(y, z)] + F_{y,a} \left[\log \log \left(1 - E(y, H(y, a)) \right) \right] \quad (1)$$

where, $F_{y,z}[\log \log E(y, z)]$ represents residual group ; $F_{y,a} \left[\log \log \left(1 - E(y, H(y, a)) \right) \right]$ indicates spatial and channel-wise importance for each feature map [16]. Pixel-level consistency is enforced using L1 loss, which quantifies absolute difference between ground truth and anticipated classification output [26]. By maintaining precise details, it aids RGCSA network in lowering artifacts and enhancing tumor classification accuracy is calculated by using,

$$L_{L1} = F_{y,z,a} [\|z - H(y, z)\|_1] \quad (2)$$

where, $F_{y,z,a}$ represents soft-max function ; Z represents spatial weight matrix ; $H(y, z)$ denotes channel weight matrix [13]. The total loss function optimizes classification accuracy, feature separation and spatial consistency by combining adversarial, L1, contrastive, and registration losses [11]. For efficient tumor detection, it guarantees that RGCSA network acquires strong and discriminative representations is given in L_{all} .

$$L_{all} = L_{adv} + \lambda_{L1} L_{L1} \quad (3)$$

where, L_{all} represents loss function for predicted class ; λ_{L1} is a fully connected layer that performs final detection [2]. The probability of going from one node to another in MRI graph is determined by Random Walk Transition Probability, which is dependent on connectedness [17, 24]. It facilitates investigation of tumor-related structures both locally and globally by modeling pathways through nearby brain regions. It's given by equation (4).

$$Q(w_k | (w_0, \dots, w_{j-1})) = 1[(w_j, w_k) \in \varepsilon_h] / E(w_j) \quad (4)$$

where, $Q(w_k | (w_0, \dots, w_{j-1}))$ represents possibility of traveling to node w_k based on walk history; $1[\cdot]$ is indicator function: equals 1 in presence of an edge, 0 otherwise; $(w_j, w_k) \in \varepsilon_h$ is presence of an edge in graph between nodes w_j and w_k ; $E(w_j)$ is degree of node w_j . Semantic Topological Walk Representation combines nodes' structural traversal pattern in graph with their feature information [1, 22]. For precise detection, this embedding improves knowledge of tumor-relevant patterns as

$$l(x) = g(\varphi_y(\omega_y(x)), \varphi_v(\omega_v(x))) \quad (5)$$

where, $l(x)$ represents combined embedding that depicts walk x ; g is

function for fusing two embeddings into a single representation; φ_y represents function for mapping semantic sequences onto latent space; $\omega_y(x)$ is semantic embedding sequence along walk x ; φ_v is topological sequence encoding mapping function into latent space; $\omega_v(x)$ is encoding topological sequences into latent space using a mapping function. The final representation of a node is created by aggregating embeddings of several random walks that conclude at that node [3, 9]. This improves precision of tumor classification in MRI graphs by capturing both local and global context. It's given by equation (6).

$$\psi(w) = \sum_{\{w\}, |x|=m, xm=w} q(x)l(x) \quad (6)$$

where, $\psi(w)$ represents node w final model utilized for detection; w is random stroll with a set length; $xm = w$ represents walk x comes to an end at node w ; $q(x)$ is statistical probability of sampling walk x ; $l(x)$ is combining topological and semantic properties to embed walk x . RGCS-NCNN technique effectively captured both semantic and structural patterns, enabling precise classification of MRI data into Tumor and Non-Tumor categories. The model consistently demonstrated improved accuracy by focusing on relevant detection features [10, 25]. After brain tumor detection, hyper-parameter $q(x)$ of RGCS-NCNN model can be optimized by using Aphid-Ant Mutualism Optimization technique [4, 19].

Aphid-Ant Mutualism Optimization

The Aphid-Ant Mutualism (AAM) algorithm is a nature-inspired metaheuristic designed to optimize high-dimensional problems by modeling cooperative behavior between aphids and ants [5, 8]. It begins by generating a mixed population of candidate solutions, mimicking natural mutualism. Aphids serve as primary search agents, while ants guide exploration and enhance diversity. This approach is particularly effective for navigating complex landscapes in detection tasks like brain tumor detection [20]. The NO is used to optimize hyperparameter $q(x)$ of RGCS-NCNN model [12].
Step 1: Initialization

In initialization phase of AAM, a population individual is randomly generated within defined variable bounds. This population is split into two groups: aphids representing candidate solutions and ants acting as support agents to guide exploration [6, 25]. Aphids explore solution space directly, while ants assist in movement and diversity enhancement. The number of aphids exceeds ants to reflect biological need for multiple aphids to support each ant's behavior. It's given by equations (7) and (8).

$$Aphid_{l,j} = MC_j + rand \times (UB_j - LB_j) \quad (7)$$

$$Ant_{q,k} = MC_j + rand \times (UB_j - LB_j) \quad (8)$$

where, $Aphid_{l,j}$ represents location of l^{th} aphid in j^{th} dimension; $Ant_{q,k}$

represents ant's position in k^{th} dimension on q^{th} dimension ; MC_j is lower limit of j^{th} variable ; $rand$ is random number between 0 and 1; UB_j is maximum value of j^{th} variable; LB_j is lower limit of j^{th} variable [14].

Step 2: Fitness Function

Every individual's solution quality (reduced error) is evaluated using fitness function. It chooses person with highest fitness value to create next. The algorithm selects optimal solutions with assist of fitness function. The objective function calculates fitness values for every potential solution during optimization. The fitness matrix, which is shown in Equation (25), is then created by combining and maintaining these values.

$$FitnessFunction = Min(q(x)) \quad (9)$$

where, $q(x)$ represents hyperparameter of detection.

Step 3: Aphids Evolution Based on Their Own Experience (Exploitation phase)

In Aphids' Evolution Based on Their Own Experience, high-performing aphids refine their positions by searching locally around their current best-known solutions. This exploitation phase intensifies search in promising regions to improve solution quality. A normally distributed random factor guides movement to ensure fine-grained updates. This strategy increases likelihood of converging to global optimum by leveraging aphids' individual knowledge. It's given by equations (10).

$$Aphid_{j,k}(u+1)^p = Aphid_{j,k}(u)^p + \alpha_1 \cdot q(x) \times \frac{randp}{u} \times (UB_j - LB_j) \quad (11)$$

where, $Aphid_{j,k}(u+1)^p$ represents present location of k^{th} aphid in j^{th} dimension at iteration u in colony p ; $Aphid_{j,k}(u)^p$ is position update in upcoming iteration ; α_1 is step size is controlled by scaling factor; $randp$ is random integer having a normal distribution ; u signifies iteration number as of right now [27].

Step 4: Aphids Movement Using Ants (Exploration Phase)

In Aphids' Movement Using Ants, weak aphids are guided by randomly selected ants to explore new areas of search space. This exploration phase enhances population diversity and assists avoid premature convergence by expanding search region. The movement is influenced by distance between aphid and ant, scaled by random factors [28]. This strategy mimics natural cooperation where ants assist aphids in reaching richer food sources. It's given by equations (12).

$$Aphid_{j,k}(u+1)^p = Ant_{rand}(u)^p + \beta \times rand \times |Aphid_{j,k}(u)^p - Ant_{rand}(u)^p| \quad (12)$$

where, $Ant_{rand}(u)^p$ represents location of a randomly chosen ant at iteration uu inside same colony; β is random number that controls strength of exploration and has a normal distribution [0,1]; $rand$ is uniformly distributed random number [0,1] that is used to scale movement; $|\cdot|$ is aphid

and ant absolute difference (Euclidean distance).

Step 5: Termination

The AAM-based hyperparameter $q(x)$ optimization dynamically adjusts for improved performance, balancing exploration and exploitation. If not, Steps 3-5 are carried out again until stopping requirements are satisfied. Figure 1 describes flow chart of an AAM.

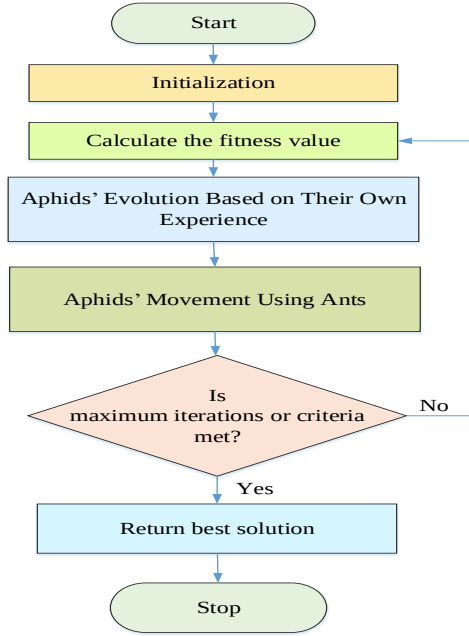


Figure 1: Flowchart of Aphid-Ant Mutualism

Results and Discussion

This section focuses on evaluating suggested RGCS-NCGNN-AAM approach for MRI image detection of brain tumor. This section discusses paper's conclusions utilizing an innovative way of analysis. The method is implemented using Python programming language. Table 1 lists all of simulation situations used by researchers for evaluation.

Table 1: Simulation parameters

Parameters	Description
Software	Python 3.7
OS	Windows 10
Data type	MRI scan
Dataset	BraTS2018, Figshare
Proposed neural network	Residual Group Channel and Space Non-Convolutional Graph Neural Network
Optimization	Aphid-Ant Mutualism

3.1 Dataset description

The process for detecting brain tumors from MRI image is explained in detail in this section. Details about input data's source, BraTS2018 [33], Figshare [34] dataset, are provided below:

3.1.1 BraTS2018 dataset

The BRATS2018 dataset [29] is a benchmark dataset comprising multi-modal MRI scans of brain tumors, specifically High-grade Glioma (HGG) and Low-grade Glioma (LGG). It includes a total of 39,835 images, with 27,035 images used for training and 12,800 for testing. The dataset consists of 29,605 HGG images (19,805 for training and 9,800 for testing) and 10,230 LGG images (7,230 for training and 3,000 for testing). It is widely used for evaluating tumor segmentation and classification models.

3.1.2 Figshare dataset

An open-access benchmark commonly used for brain tumor classification tasks in medical imaging research is taken from Figshare dataset [30]. It includes MRI scans that are separated into three tumor types: pituitary, meningioma, and glioma. In particular, dataset contains 1464 images of pituitary tumors, 708 images of meningioma and 1426 images of gliomas. To make process of creating and testing models more efficient, these are divided into subsets for training and testing. The data set enables robust validation of Directed Acyclic Graph Sample and Aggregate Neural Network models for brain tumor detection and is compatible with supervised learning techniques. Table 2 lists training & testing values in detail.

Table 2: Training and testing values in dataset

Dataset	Classes	Total No. of Images	Training	Testing
Total No. of Images BraTS2018: 39,835				
BraTS2018	High-Grade Glioma	29,605	19,805	9,800
	Low-Grade Glioma	10,230	7,230	3,000
Total No. of Images Figshare: 3,598				
Figshare	Glioma	1426	1070	356
	Meningioma	708	531	177
	Pituitary	1464	531	766

Table 2 presents the training and testing values in dataset. There are 39,835 images in BraTS2018, which are divided into 29,605 and 10,230 images with High-Grade Glioma and Low-Grade Glioma classes, respectively. 3,598 images in Figshare are divided into three tumor types: pituitary, glioma, and meningioma. To guarantee reliable model evaluation, each dataset is separated into training and testing sets. With this configuration, model can efficiently learn about gliomas and generalize to different kinds and levels of complexity of brain tumors.

3.2 Performance metrics

The efficiency of suggested RGCS-NCNN-AAM approach is evaluated using an Accuracy, Precision, Recall, False-Positive Rate (FPR), True

Negative Rate (TNR), F1-Score and ROC. Several recognized methods are applied to compare these metrics [30]. Table 3 shows these Performance metrics.

Table 3: Performance metrics

Metrics	Equation
Accuracy	$\frac{TP + TN}{TP + TN + FP + FN}$
Recall	$\frac{TP}{TP + FN}$
Precision	$\frac{TP}{TP + FP}$
FPR	$\frac{FP}{FP + TN}$
TNR	$\frac{TN}{TN + FP}$
F1-score	$\frac{2 \times precision \times Recall}{precision + Recall}$

True Positive (TP): Correctly detects tumor in an MRI that actually has a tumor.

True Negative (TN): Correctly identifies an MRI as non-tumor when there is no tumor present.

False Positive (FP): Incorrectly classifies a non-tumor MRI as having a tumor.

False Negative (FN): Fails to detect a tumor in an MRI that actually contains a tumor.

3.3 Performance Analysis of Proposed Model

The effectiveness of suggested model is assessed using two different datasets, BraTS2018 and Figshare, with an emphasis on important detection criteria. Accuracy, TNR, ROC and F1-score are evaluated to give a complete image of model's efficacy. These measures demonstrate model's accuracy in tumor type detection, training convergence and cross-class differentiation resilience. Additional evidence of model's strong and reliable detection abilities can be found in performance metrics like recall, precision and FPR. Brats2018 and Figshare datasets image results are displayed in Tables 4 and 5.

Table 4: Image outcome on BraTS2018 dataset

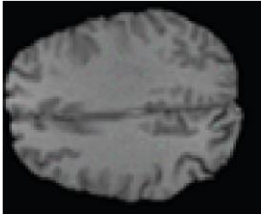
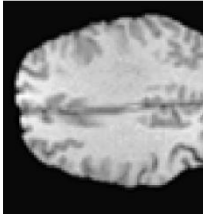
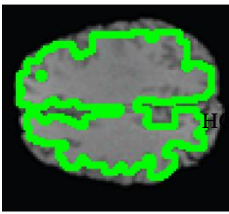
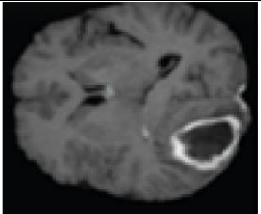
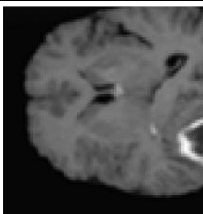
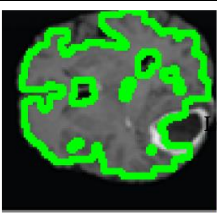
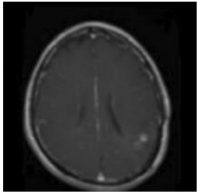
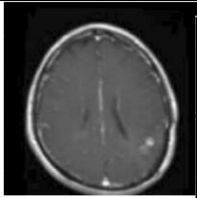
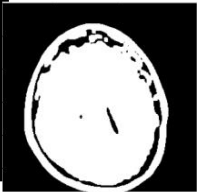
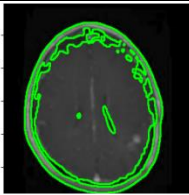
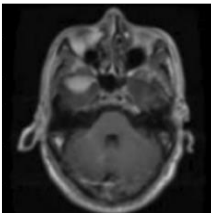
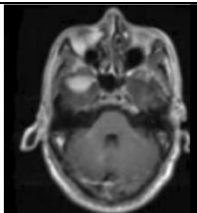
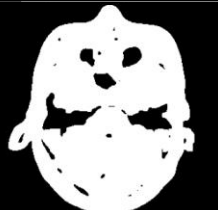
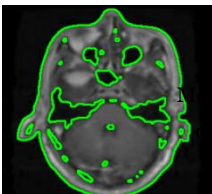
Input image	Preprocessed image	Segmented image	Feature reduction image	Class
				HGG
				LGG

Table 5: Image outcome on Figshare dataset

Input image	Preprocessed image	Segmented image	Feature reduction image	Class
				Glioma
				Meningioma

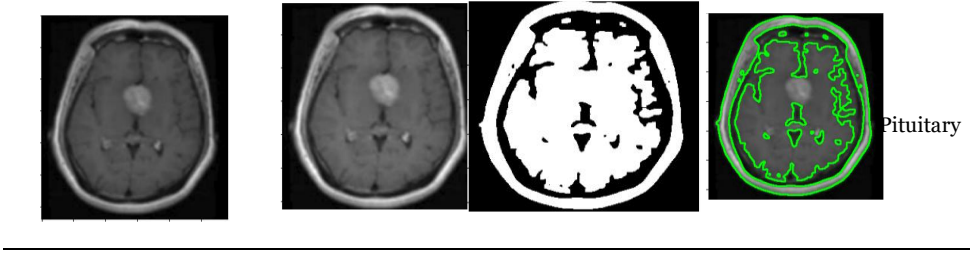


Image results from BraTS2018 and Figshare datasets are displayed in tables 4 and 5. The raw MRI image, its preprocessed form, feature extraction and segmented tumor region are all included in each row. The model's detection accuracy is demonstrated by identified tumor classes: HGG and LGG for BraTS2018 and Glioma, Meningioma and Pituitary for Figshare.

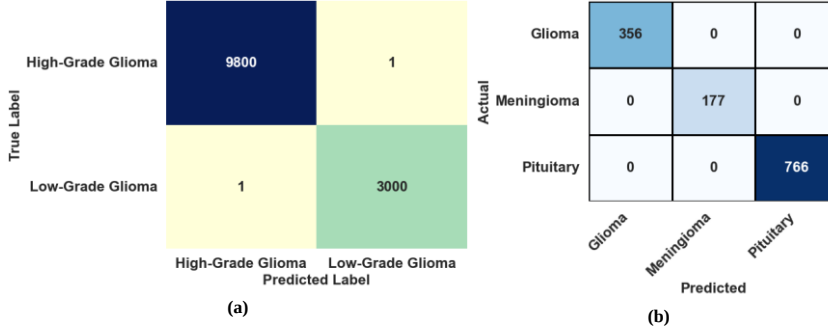


Figure 2: Proposed confusion matrix for (a) BraTS2018 and (b) Figshare Datasets

Figure 2(a) shows results are classified as either High-Grade Glioma or Low-Grade Glioma. There was just one incorrect classification in each category, with model correctly classifying 3000 low-grade and 9800 high-grade glioma instances. This shows that two glioma kinds can be distinguished almost perfectly, indicating extremely accurate performance. In figure 2(b) shows performance of multiclass classification for pituitary, meningioma, and glioma tumors. There were no misclassifications and all classes were accurately predicted, indicating that three tumor types were perfectly classified.

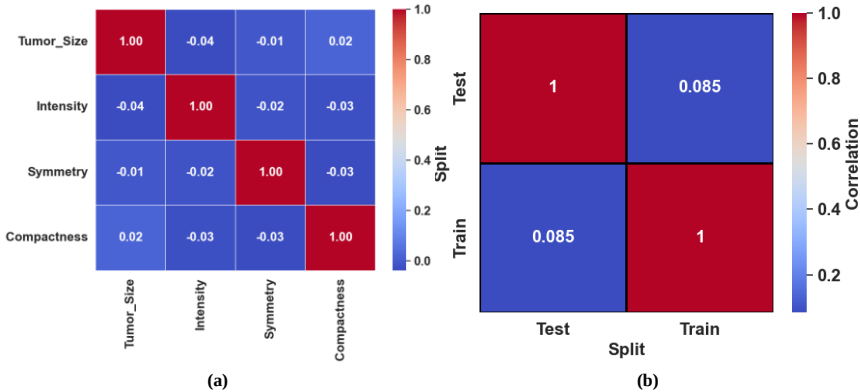


Figure 3: Proposed correlation matrix for (a) BraTS2018 and (b) Figshare Datasets

Figure 3(a) shows feature correlation among Tumor Size, Intensity, Symmetry, and Compactness. All diagonal values are 1.00, indicating perfect self-correlation. Off-diagonal values are close to zero, suggesting negligible correlation between different features, which supports independence of each extracted feature for classification tasks. Figure 3(b) shows connections between testing and training datasets. Within same split, complete correlation is indicated by diagonal values of 1.0. The little data leakage and strong generalization between training and testing subsets are confirmed by cross-correlation value of 0.085.

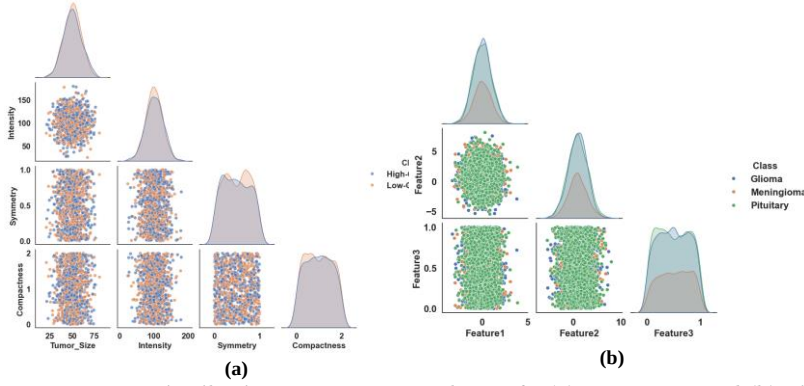


Figure 4: Feature Distribution across Tumor Classes for(a) BraTS2018and (b) Figshare Datasets

Figure 4(a) shows feature distribution differences between high-grade and low-grade gliomas in terms of tumor size, intensity, symmetry and compactness. Although there are minor differences, overlapping distributions show that traits are distributed similarly across two classes. For glioma grading, aid in visualizing feature dispersion and class separability. In figure 4(a) shows three retrieved traits among tumor types of pituitaries, glioma and meningioma. While diagonal histograms display distribution of individual features, each scatter-plot illustrates relationship between feature pairs. The graphic supports multiclass classification analysis by shedding light on feature overlap and dissemination across tumor types.

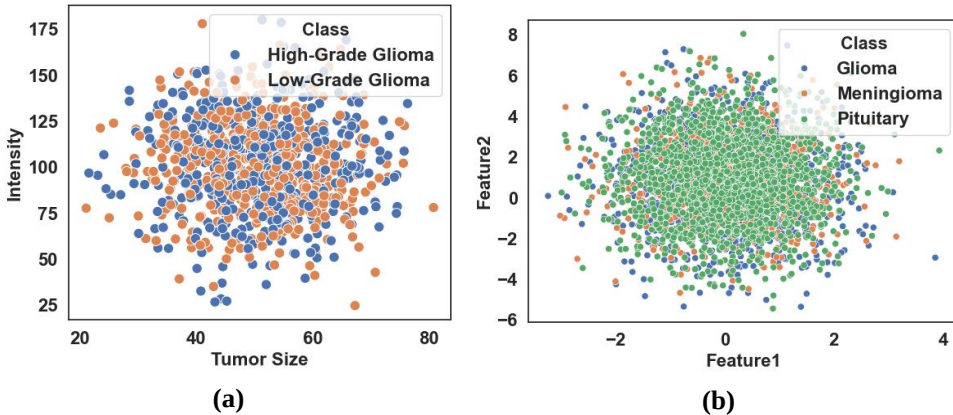


Figure 5: Two-Dimensional Feature Space Representation for(a) BraTS2018and (b) Figshare Datasets

Figure 5(a) shows correlation between size of tumor and its intensity for both high and low-grade glioma samples. Although characteristics offer some differentiation across classes, points' partial overlap suggests that more dimensionality reduction and sophisticated modeling can be necessary for best classification results. In figure 5(b) shows samples from pituitary tumors, meningioma and gliomas employing features 1 and 2. The classes are not linearly separable, as indicated by dense and overlapping distribution of dots, which raises possibility that precise multiclass classification can demand complicated boundaries and other properties.

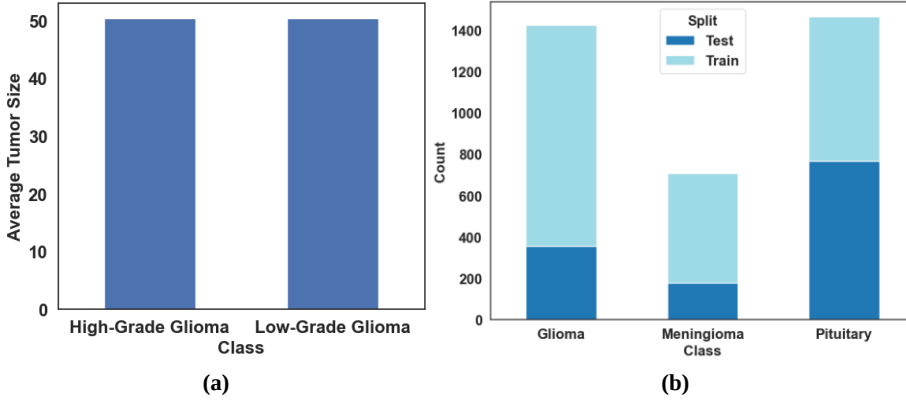


Figure 6: Class-Wise Distribution Analysis of Tumor Size and Sample Count for (a) BraTS2018 and (b) Figshare Datasets

Figure 6(a) shows typical tumor size of gliomas of high and low grades. Tumor size alone cannot be a viable differentiating criterion for glioma grading; rather, it can need to be supplemented with other features. This is demonstrated by nearly equal average sizes of two groups. In figure 6(b) shows number of test and training samples for three tumor classes (pituitary, meningioma and glioma). Because distribution is evenly distributed among splits, accurate performance evaluation is guaranteed. The classification robustness for this category can be positively impacted by large number of pituitary samples in test set.

Figure 7(a) shows intensity value distribution for cases of high- and low-grade gliomas. The data point's exhibit comparable intensity patterns for both classes and are symmetrically distributed with some overlap. This implies that for accurate glioma classification, intensity alone cannot have much discriminative value and combined with additional features.

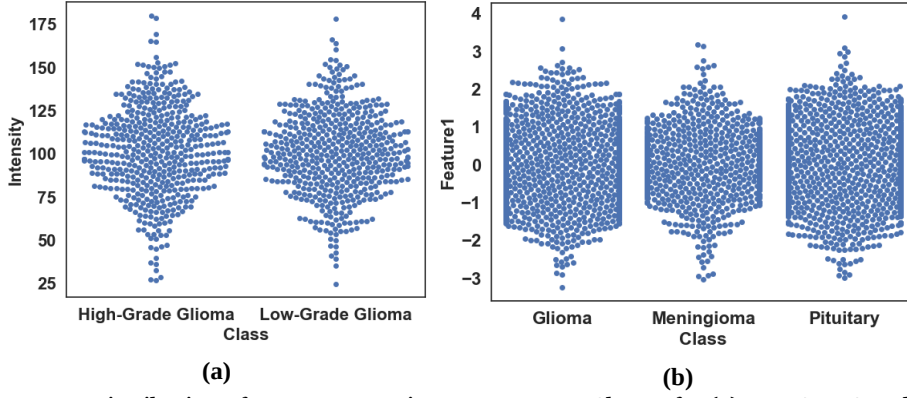


Figure 7: Distribution of Feature Intensity across Tumor Classes for (a) BraTS2018 and (b) Figshare Datasets

In figure 7(b) shows distribution of Feature1 in pituitary, glioma, and meningioma cancers. Similar ranges and densities across classes indicate possible feature overlap. To increase tumor classification performance and class separation, more or altered characteristics can be required.

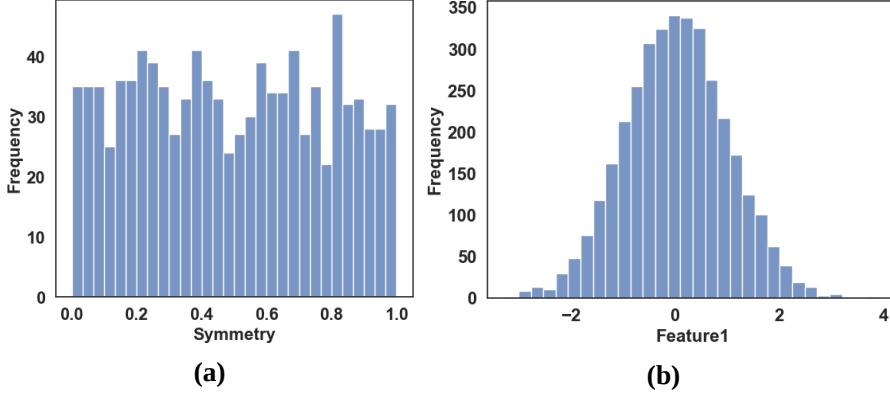


Figure 8: Frequency Distribution of Tumor-Related Features for (a) BraTS2018 and (b) Figshare Datasets

Figure 8(a) shows symmetry feature's frequency distribution. Indicating that symmetry values are widely distributed and contribute equally to model training without favoring any particular value range, distribution is comparatively uniform over 0-1 range. In figure 8(b) shows feature1's distribution is a bell-shaped, almost normal curve with zero at its center. This implies that feature has undergone standardization and, by preserving a constant scale and distribution, can improve learning stability in classification models.

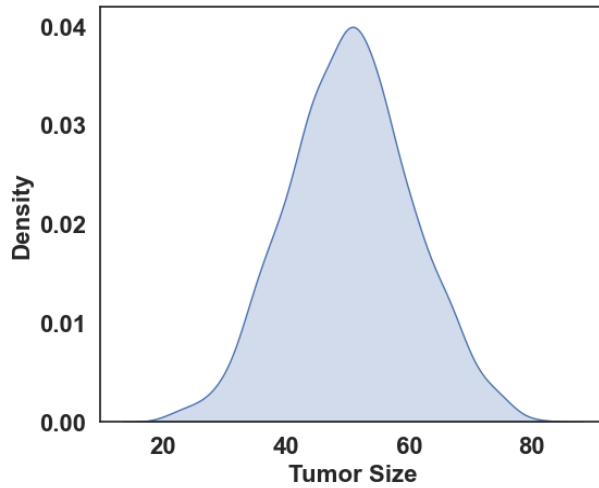


Figure 9: Kernel Density Estimation of Tumor Size Distribution for BraTS2018Dataset

Figure 9 shows tumor size density distribution for each sample. Tumor sizes are roughly regularly distributed, according to smooth curve, with majority of values centered on 50-point range.

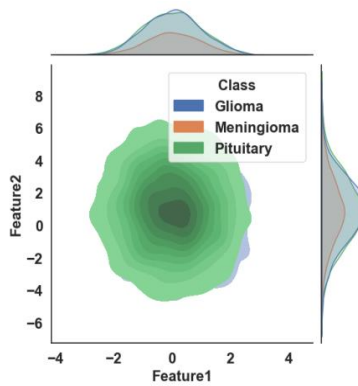


Figure 10: Joint Density and Marginal Distribution of Extracted Tumor Features for Figshare Dataset

There can be fewer extreme occurrences, as tails taper out toward smaller and larger sizes. This balanced distribution lessens possibility of bias toward tumors of particular sizes during training and can aid deep learning models in generalizing better during classification. Figure 10 shows contours between Features 1 and 2 for three types of brain tumors: pituitary, glioma, and meningioma. There are difficulties with distinct separability, as

indicated by central overlapping zones, which imply that feature distributions are densely packed. Individual feature distribution by class is displayed in axes' marginal density plots. Given overlap in both dimensions, it can be necessary to include more discriminative features in order to increase accuracy of multiclass classification.

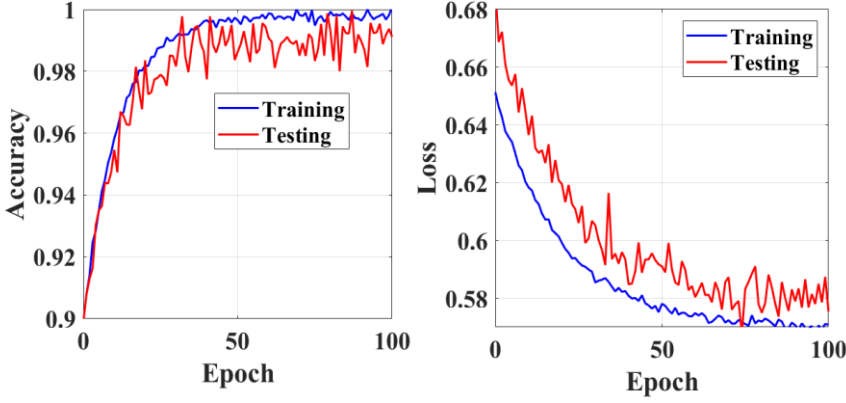


Figure 11: Proposed (a) Accuracy and (b) Loss graph for BraTS2018Dataset

Figure 11 (a) shows both training and testing accuracy increase steadily over epochs, eventually stabilizing near 1.0. This indicates that model has effectively learned from data and generalizes well to unseen samples, with minimal performance gap between training and testing curves. In figure 11 (b) shows steady drop in loss values for testing and training. Although there are some little variations in testing curve, general downward trend verifies model's steady convergence and effective long-term prediction error minimization.

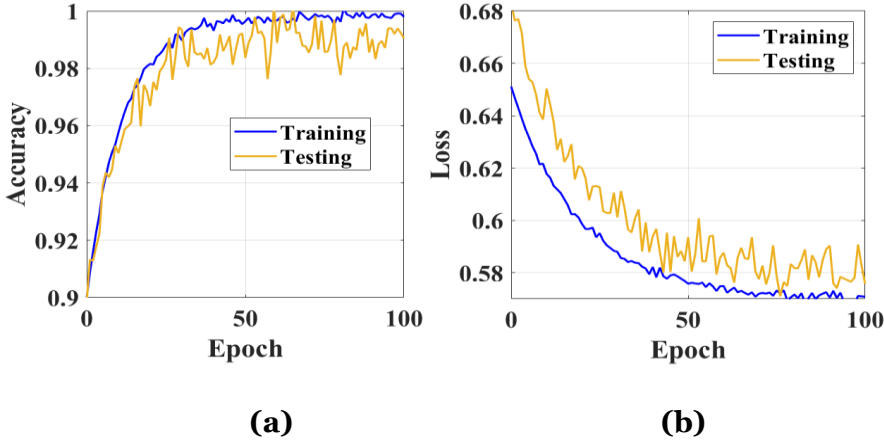


Figure 12: Proposed (a) Accuracy and (b) Loss graph for Figshare Dataset

Figure 12 (a) shows model's learning process over a hundred epochs. The accuracy of training and testing increases progressively, with training accuracy being somewhat higher in later epochs. This model performs well in classification, achieving almost 100% accuracy. Training and testing accuracy closely match, indicating efficient generalization without appreciable over-fitting. In figure 13 (b) shows training and testing loss gradually decreased during course of 100 epochs. While testing loss also exhibits a declining trend with little variations, training loss continuously

declines. With few indications of over-fitting, this trend shows that model is learning efficiently and reducing prediction error.

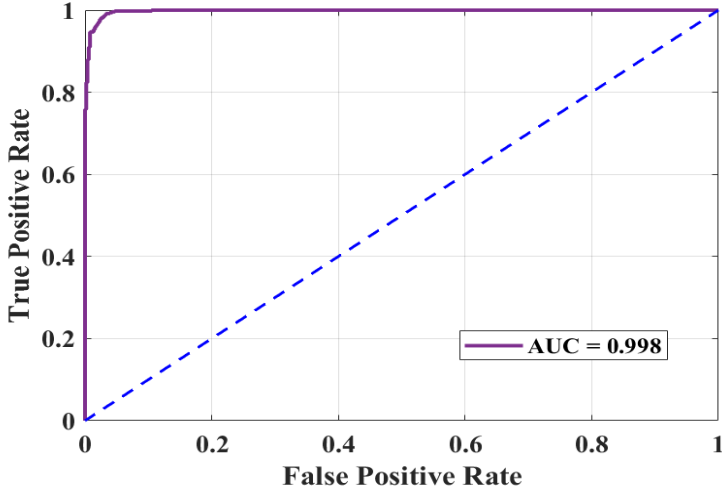


Figure 13: ROC curve forBraTS2018 Dataset

Figure 13 shows trade-off between false-positive and true-positive rates at different threshold levels. Better model performance is indicated by a curve that is closer to upper-left corner. With a reported Area under the Curve (AUC) of 0.998, discriminative ability is excellent. The model appears to effectively distinguish between classes, reaching high sensitivity and specificity with few erroneous classifications, as seen by nearly flawless AUC score. Random guessing is represented by diagonal reference line.

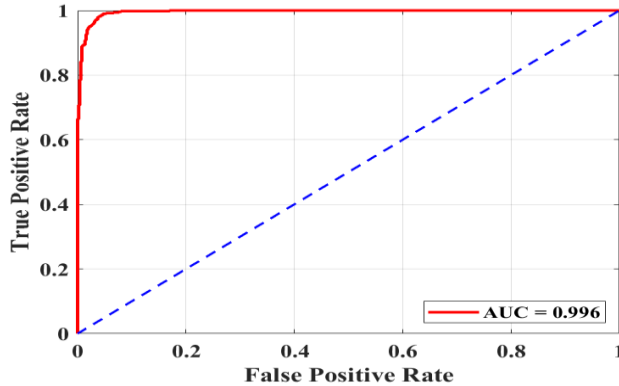


Figure 14: ROC curve Forfarshire Dataset

Figure 14 shows true positive rate against false positive rate is how Receiver Operating Characteristic (ROC) curve assesses model's classification ability. High sensitivity and a low false positive rate are shown by curve's fast climb toward top-left. The model's exceptional capacity to differentiate across classes is demonstrated by its Area under the Curve (AUC) score of 0.996. The baseline for random detection performance is shown by dashed diagonal line.

3.4 Comparative analysis

The Accuracy, Precision, Recall, FPR, TNR, F1-Score and ROC are among

key metrics used to assess performance of suggested RGCS-NCGNN-AAM architecture for brain tumor detection. To compare performance of framework, two popular methods are used: BraTS2018 dataset and Figshare dataset. ADHDC-Net [16], 2DU-Net- SSD [17], PLS [18], SGLDM-HHO [19] and SOTA-ResUNet+ [20] are compared to proposed model on BraTS2018 dataset, while DCNN-GD [21], DaSAM-ResNet [22], CNN-VGG16 [23], MANet [24] and EDet-BTR [25] are evaluated on Figshare dataset. The performance comparison on BraTS2018 and Figshare datasets are displayed in Tables 6 and 7.

Table 6: Comparison of performance on the BraTS2018 dataset

Methods	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	TNR (%)	FPR (%)
ADHDC-Net [16]	85	78	80	83	81	0.14
2DU-Net- SSD [17]	87	82	77	84	83	0.16
PLS [18]	82	77	74	78	81	0.22
SGLDM-HHO [19]	88	83	82	85	84	0.21
SOTA-ResUNet+ [20]	85	78	83	81	83	0.17
RGCS-NCGNN-AAM (Proposed Method)	90.94	90.75	90.79	90.84	90.80	0.04

Table 6 displays effectiveness of various methods for using BraTS2018 dataset to brain tumor detection. The proposed method outperforms previous approaches by achieving its highest accuracy (90.94%), recall (90.79%), precision (90.75%), F1-score (90.82%), TNR (90.80%) and FPR (0.04%). However, PLS [18] technique has lower metrics, with 77% precision, 74% recall and 0.22% FPR. Additionally, proposed strategy shows its improved ability to brain tumor detection.

Methods	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	TNR (%)	FPR (%)
DCNN-GD [21]	83	80	78	80	83	0.12
DaSAM-ResNet[22]	84	83	80	81	79	0.13
CNN-VGG16 [23]	87	84	85	85	78	0.18
MANet [24]	81	75	74	77	81	0.17
EDet-BTR[25]	82	79	80	78	80	0.15
RGCS-NCGNN-AAM (Proposed Method)	90.91	90.72	90.76	90.81	90.77	0.06

Table 7: Performance comparison on Figshare dataset

Table 7 compares effectiveness of various methods for detecting brain

tumors on Figshare dataset. The proposed approach achieves 90.91% accuracy, 90.72% precision, 90.81% F1-score, 90.76% recall, 90.77 TNR and 0.06% FPR, outperforming all other approaches in every category. Conversely, MANet [24] attains 75% precision, 74% recall, and 0.17 FPR fortunately with greater mistake rates.

3.5 Statistical analysis

The statistical significance of observed differences between groups is assessed by statistical analysis. It assists in determining if differences in outcomes are caused by real impacts as opposed to chance changes. The complexity and irregularity of shapes and patterns in an image are described by a quantitative metric called Fractal Dimension (FD). By catching minute details that conventional geometric metrics can miss, it aids in assessment of structural differences. FD is frequently used in medical imaging to examine tissue textures and spot anomalies. In general, more complex or diverse structures are indicated by higher FD values. Table 9 shows Average Tumor FD versus Non tumor FD Comparison.

Table 8 displays tumor and nontumor Fractal Dimensions (FD) across resolutions using Linear Algebra with Steerable Transformer (LA-ST), Residual Group Channel and Space Non-Convolutional Graph Neural Network (RGCS-NCGNN), and Aphid-Ant Mutualism (AAM) techniques. LA-ST shows limited significance, with differences only at 16×16 and 64×64. RGCS-NCGNN achieves consistent significance at most resolutions, highlighting strong separation capabilities. AAM shows no difference at 8×8 but performs significantly better at higher resolutions.

Table 8: Average Tumor FD versus Non tumor FD Comparison

Algorithm	Resolution	Average Tumor FD (mean ± s _x)	Average Nontumor FD (mean ± s _x)	Significant Difference
LA-ST	8×8	2.520 ± 0.120	2.530 ± 0.100	None
	16×16	3.080 ± 0.150	3.110 ± 0.100	P < .05
	32×32	3.170 ± 0.160	3.170 ± 0.110	None
	64×64	2.100 ± 0.110	2.130 ± 0.070	P < .05
RGCS-NCGNN	8×8	2.670 ± 0.170	2.780 ± 0.080	P < .01
	16×16	3.180 ± 0.230	3.240 ± 0.070	P < .01
	32×32	3.320 ± 0.270	3.320 ± 0.110	None
	64×64	3.990 ± 0.150	4.020 ± 0.090	P < .05
AAM	8×8	2.560 ± 0.170	2.600 ± 0.160	None
	16×16	2.630 ± 0.180	2.690 ± 0.170	P < .01
	32×32	2.790 ± 0.180	2.870 ± 0.150	P < .01
	64×64	3.300 ± 0.340	3.410 ± 0.210	P < .01

3.6 Ablation study

In ablation study, each element of suggested RGCS-NCGNN-AAM technique for detection of braintumor based on MRI images was assessed for its impact. The study carefully evaluated if changing particular model components affected model's overall performance. The ablation results are displayed in Table 9.

Table 9: Ablation outcomes

Methods	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
Performance metrics	Accuracy (%)	Accuracy (%)	F1-score (%)	F1-score (%)
NCGNN	96.57	97.55	93.33	95.49
RGCS-NCGNN	95.41	98.65	98.82	94.67
RGCS-NCGNN-AAM	95.94	98.91	98.84	94.81

Table 9 demonstrates accuracy and F1-score of three approaches Non-Convolutional Graph Neural Network (NCGNN), Residual Group Channel and Space Non-Convolutional Graph Neural Network (RGCS-NCGNN) and Residual Group Channel and Space Non-Convolutional Graph Neural Network withAphid-Ant Mutualism (RGCS-NCGNN-AAM) assessed on Figshare and BraTS2018 datasets. In both datasets, RGCS-NCGNN-AAMperforms best, achieving accuracy and F1-scores close to 95%, this suggests superior segmentation abilities. Despite DAGNN's high performance, RGCS-NCGNN and its improved version RGCS-NCGNN-AAM outperform it. For splitting brain tumors tasks, results demonstrate how well Aphid-Ant Mutualism (AAM) increases model precision and dependability.

3.7 Discussion

The proposed RGCS-NCGNN-AAM method achieved outstanding numerical results across multiple evaluation parameters, demonstrating its effectiveness in brain tumor detection using MRI images. The model outperformed other models such as SGLDM-HHO (88% accuracy) and 2DU-Net-SSD (87% accuracy) on BraTS2018 dataset, achieving a peak accuracy of 95.94% and an F1-score of 98.84%. Its resilience in multi-class classification was further confirmed by its 98.91% accuracy and 94.81% F1-score for Figshare dataset, all while maintaining a minimal false positive rate (FPR) of 0.06%.The efficacy of model was further confirmed by Fractal Dimension (FD) study, which revealed that, particularly at higher resolutions, RGCS-NCGNN and AAM separated tumor and non-neoplastic regions statistically significantly. Significant gains were also observed in F1-score, suggesting improved memory and precision balance.The model's exceptional discriminative performance was further demonstrated by ROC curves, which verified near-perfect classification with AUC scores of 0.998 (BraTS2018) and 0.996 (Figshare).

Conclusion

The proposed RGCS-NCGNN-AAM framework integrates cutting-edge techniques at every stage of processing, successfully addressing main obstacles in dimensions reduction-based brain tumor identification. The model guarantees correct spatial representation by using SD-PCA to preserve important tumor-related characteristics and LABF for noise-resilient pre-processing. By incorporating topological and semantic links, RGCS-NCGNN ensures robust classification, while LA-ST segmentation technique further improves boundary precision. Lastly, AAM optimization improves convergence and generalization by adaptively adjusting model parameters. When it comes to tumor detection from intricate MRI datasets, our comprehensive pipeline exhibits excellent accuracy, dependability and scalability. High-precision brain tumor detection is ensured by suggested RGCS-NCGNN-AAM framework, which optimizes model performance using adaptive bio-inspired techniques while maintaining important spatial properties. The RGCS-NCGNN-AAM model multi-stage processing and bio-inspired optimization result in an increase in computational complexity. Future developments will add Quantum Graph Neural Networks (QGNs) to suggested RGCS-NCGNN-AAM framework to improve topological and spatial learning effectiveness while lowering computational cost. Utilizing unlabelled MRI data, self-supervised contrastive learning will be used to improve generalization across various clinical datasets. Convergence will be accelerated and strengthened by incorporating a Hybrid Swarm–Quantum Mutualism model into optimization approach.

The RGCS-NCGNN-AAM framework offers significant clinical value by assisting radiologists and oncologists in making faster, more accurate diagnoses of brain tumors. By preserving critical spatial and structural details through SD-PCA and LABF preprocessing, the model ensures reliable identification of tumor boundaries and grades, which are essential for assessing tumor aggressiveness. The enhanced segmentation and classification precision support clinicians in determining appropriate treatment strategies, such as surgical planning, radiotherapy targeting, or chemotherapy decisions. While the model demonstrates strong performance on research datasets like BraTS and Figshare, future work should focus on validating its effectiveness using real-world clinical data to ensure broader generalization and practical applicability across diverse healthcare settings.

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